

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1. (Currently amended) A method for preventing or treating HIV infection in a human, said method comprising:

a) ~~screening a plurality of cells from a human donor to identify stem cells having a beneficial gene, wherein the beneficial gene is a polymorphism in a CCR5 gene; and~~

b) transplanting said ~~stem cells~~ into the human a stem cell-rich population of cells from a human donor, wherein the stem cell-rich population of cells has a beneficial gene that is a polymorphism in a CCR5 gene, thereby preventing or treating said HIV infection.

2-14. (Cancelled)

15. (Previously presented) The method of claim 1, wherein said polymorphism is a 32 basepair deletion in the coding region.

16. (Previously presented) The method of claim 1, wherein said polymorphism is CCR5m303.

17. (Previously presented) The method of claim 1, wherein said polymorphism is in the promoter region of CCR5.

18. (Currently amended) The method of claim 1, wherein said ~~plurality stem cell-rich population of cells are obtained~~ is selected from the group consisting of embryos, bone marrow, peripheral blood, placental blood, umbilical cord blood, and adipose tissue.

19. (Cancelled)

20. (Currently amended) The method of claim 1, wherein said method further comprises identification of the HLA genotype or phenotype of said ~~stem cells~~ stem cell-rich population of cells.

21-23. (Cancelled)

24. (Currently amended) The method of claim 1, ~~wherein said screening comprises identification of stem cells with said beneficial gene~~ further comprising a step of screening a cell sample from a human donor to identify the stem cell-rich population of cells that has a polymorphism in the CCR5 gene.

25. (Currently amended) The method of claim 24, wherein said ~~beneficial gene~~ polymorphism in the CCR5 gene is detected using a hybridization-based assay, a sequencing assay, or a functional assay.

26. (Cancelled)

27. (Currently amended) The method of claim 1, wherein said ~~plurality stem cell-rich population of cells are~~ is obtained from umbilical cord blood.

28. (New) The method of claim 24, wherein said method further comprises  
b) identification of an HLA genotype or phenotype of said stem cell-rich population of cells.

29. (New) The method of claim 28, wherein said identification of the HLA genotype is via a high-throughput method using allele-specific primers and HLA locus-specific capture oligonucleotides immobilized on a solid phase.

30. (New) The method of claim 28, wherein said method further comprises  
c) identification of an HLA genotype or phenotype of said human.

31. (New) The method of claim 28, wherein said HLA genotype or phenotype of said stem cell-rich population of cells is compatible with said HLA genotype or phenotype of said human.